

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/520, 299  
Source: PCT  
Date Processed by STIC: 01/31/2006

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 01/31/2006

PATENT APPLICATION: US/10/520,299

TIME: 15:48:25

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Output Set: N:\CRF4\01312006\J520299.raw

3 <110> APPLICANT: Rupp, Fabio  
 4 Wang, Jianrui  
 5 Zhou, Ping  
 6 Wehrman, Tom  
 7 Wang, Zhiwei  
 8 Tang, Y. Tom

10 <120> TITLE OF INVENTION: Methods and Materials Relating to Novel Polypeptides and Polynucleotides

12 <130> FILE REFERENCE: HYS-B2 PCT

C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/520,299

C--> 15 <141> CURRENT FILING DATE: 2005-01-04

17 <150> PRIOR APPLICATION NUMBER: PCT/US02/29636

18 <151> PRIOR FILING DATE: 2002-09-18

20 <150> PRIOR APPLICATION NUMBER: 60/395,402

21 <151> PRIOR FILING DATE: 2002-07-12

23 <150> PRIOR APPLICATION NUMBER: PCT/US02/22858

24 <151> PRIOR FILING DATE: 2002-07-19

26 <150> PRIOR APPLICATION NUMBER: 10/112,944

27 <151> PRIOR FILING DATE: 2002-03-28

29 <150> PRIOR APPLICATION NUMBER: 60/306,971

30 <151> PRIOR FILING DATE: 2001-07-21

32 <150> PRIOR APPLICATION NUMBER: 10/296,115

33 <151> PRIOR FILING DATE: 2002-11-18

35 <150> PRIOR APPLICATION NUMBER: PCT/US00/35017

36 <151> PRIOR FILING DATE: 2000-12-22

38 <150> PRIOR APPLICATION NUMBER: 09/488,725

39 <151> PRIOR FILING DATE: 2000-01-21

41 <150> PRIOR APPLICATION NUMBER: 60/418,132

42 <151> PRIOR FILING DATE: 2002-10-11

44 <150> PRIOR APPLICATION NUMBER: PCT/US02/39555

45 <151> PRIOR FILING DATE: 2002-12-10

47 <150> PRIOR APPLICATION NUMBER: 60/365,091

48 <151> PRIOR FILING DATE: 2002-03-14

50 <150> PRIOR APPLICATION NUMBER: 60/425,158

51 <151> PRIOR FILING DATE: 2002-11-08

53 <150> PRIOR APPLICATION NUMBER: 60/323,349

54 <151> PRIOR FILING DATE: 2001-09-18

56 <150> PRIOR APPLICATION NUMBER: 09/552,317

57 <151> PRIOR FILING DATE: 2000-04-25

59 <150> PRIOR APPLICATION NUMBER: 10/275,027

60 <151> PRIOR FILING DATE: 2002-10-30

62 <150> PRIOR APPLICATION NUMBER: PCT/US01/02623

63 <151> PRIOR FILING DATE: 2001-01-25

65 <150> PRIOR APPLICATION NUMBER: 09/560,875

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66 <151> PRIOR FILING DATE: 2000-04-27  
68 <150> PRIOR APPLICATION NUMBER: 10/220,366  
69 <151> PRIOR FILING DATE: 2002-08-28  
71 <150> PRIOR APPLICATION NUMBER: PCT/US01/04927  
72 <151> PRIOR FILING DATE: 2001-02-26  
74 <150> PRIOR APPLICATION NUMBER: 09/577,409  
75 <151> PRIOR FILING DATE: 2000-05-18  
77 <150> PRIOR APPLICATION NUMBER: 09/515,126  
78 <151> PRIOR FILING DATE: 2000-02-28  
80 <150> PRIOR APPLICATION NUMBER: PCT/US01/04941  
81 <151> PRIOR FILING DATE: 2001-03-05  
83 <150> PRIOR APPLICATION NUMBER: 09/574,454  
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86 <150> PRIOR APPLICATION NUMBER: 09/519,705  
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90 <151> PRIOR FILING DATE: 2002-09-27  
92 <150> PRIOR APPLICATION NUMBER: 10/273,573  
93 <151> PRIOR FILING DATE: 2002-10-18  
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105 <151> PRIOR FILING DATE: 2002-04-18  
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122 <150> PRIOR APPLICATION NUMBER: PCT/US01/02687  
123 <151> PRIOR FILING DATE: 2001-01-25  
125 <150> PRIOR APPLICATION NUMBER: PCT/US01/08631  
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132 <151> PRIOR FILING DATE: 2000-03-31  
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138 <151> PRIOR FILING DATE: 2001-05-16

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140 &lt;150&gt; PRIOR APPLICATION NUMBER: 09/577,408

141 &lt;151&gt; PRIOR FILING DATE: 2000-05-18

143 &lt;150&gt; PRIOR APPLICATION NUMBER: 10/221,279

144 &lt;151&gt; PRIOR FILING DATE: 2003-05-28

146 &lt;160&gt; NUMBER OF SEQ ID NOS: 110

148 &lt;170&gt; SOFTWARE: PatentIn version 3.1

150 &lt;210&gt; SEQ ID NO: 1

151 &lt;211&gt; LENGTH: 1222

152 &lt;212&gt; TYPE: DNA

153 &lt;213&gt; ORGANISM: Homo sapiens

155 &lt;220&gt; FEATURE:

156 &lt;221&gt; NAME/KEY: misc\_feature

157 &lt;222&gt; LOCATION: (392)..(1008)

158 &lt;223&gt; OTHER INFORMATION:

W--&gt; 161 &lt;400&gt; 1

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162 cagatcctca tctccctggg tagtgaggct catcacagac aagcaaccaa ctgctgggct      60
164 gccggtgccc cccatgttgg aacctgagtt ggagattatc tcctaagcag atacctgctt      120
166 ccaaactggg gatgtagggc ttggaaacta aaaaatgcc aagttggcag gggtgtgttc      180
168 acaagtccag caatacacag agctctgtgt attcagaggg aagttggcag gggtgtgttc      240
170 gggcagagaa actccgagtg gtacaaaggg gacgtgcccc gagtggagaa atcatgctaa      300
172 ttgtctgcac tagagctgga gaacgccacc caaatgaag agagaaaggg gagccctgtc      360
174 cagagcctcc agggccctgc gccttgctcc ttttgtctac cttcttctga tccagacaga      420
176 ccccttgagg ggggtgaaca tcaccagccc cgtgcgctg atccatggca ccgtggggaa      480
178 gtcggctctg ctttctgtgc agtacagcag taccagcagc gacaggcctg tagtgaagtg      540
180 gcagctgaag cgggacaagc cagtgaaccgt ggtgcagtcc attggcacag aggtcatcgg      600
182 caccctgcgg cctgactatc gggaccgtat ccgactcttt gaaaatggct ccctgcttct      660
184 cagcgacctg cagctggccg atgagggcac ctatgaggtc gagatctcca tcaccgacga      720
186 caccttcact ggggagaaga ccatcaacct tactgtagat gtgcccattt cgaggccaca      780
188 ggtgttgagg gcttcaacca ctgtgctgga gctcagcgag gccttcacct tgaactgctc      840
190 acatgagaat ggcaccaagc ccagctacac ctggctgaag gatggcaagc ccctcctcaa      900
192 tgactcgaga atgctcctgt ccccgacca aaagggtgctc accatcaccg gcgtgctcat      960
194 ggaggatgac gacctgtaca gctgcgtggg ggaaaacccc atcaaccagg gccggaccct      1020
196 gccttgtaag atcaccgaat acagaaaaag ctccctttca tcaatttggc tccaggaggc      1080
198 attttcctcc ttgggacctt ggtgaagacc tggccaacaa gggaaaaccc cgtctttatt      1140
200 aaaaatacaa aaaatgcccc cgctttgggt gtaagggcct gttttccgcg gcccttcggg      1200
202 aggttttgaa cagtaaattc cc                                     1222

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205 &lt;210&gt; SEQ ID NO: 2

206 &lt;211&gt; LENGTH: 823

207 &lt;212&gt; TYPE: DNA

208 &lt;213&gt; ORGANISM: Homo sapiens

210 &lt;220&gt; FEATURE:

211 &lt;221&gt; NAME/KEY: CDS

212 &lt;222&gt; LOCATION: (50)..(817)

213 &lt;223&gt; OTHER INFORMATION:

W--&gt; 216 &lt;400&gt; 2

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217 gtcagtaatt ccttggtcga cgatttcgtg ctggagaacg ccacccaaa atg aag aga      58
218                                     Met Lys Arg
219                                     1
221 gaa agg gga gcc ctg tcc aga gcc tcc agg gcc ctg cgc ctt gct cct      106

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222 Glu Arg Gly Ala Leu Ser Arg Ala Ser Arg Ala Leu Arg Leu Ala Pro
223      5                      10                      15
225 ttt gtc tac ctt ctt ctg atc cag aca gac ccc ctg gag ggg gtg aac      154
226 Phe Val Tyr Leu Leu Leu Ile Gln Thr Asp Pro Leu Glu Gly Val Asn
227 20                      25                      30                      35
229 atc acc agc ccc gtg cgc ctg atc cat ggc acc gtg ggg aag tcg gct      202
230 Ile Thr Ser Pro Val Arg Leu Ile His Gly Thr Val Gly Lys Ser Ala
231      40                      45                      50
233 ctg ctt tct gtg cag tac agc agt acc agc agc gac agg cct gta gtg      250
234 Leu Leu Ser Val Gln Tyr Ser Ser Thr Ser Ser Asp Arg Pro Val Val
235      55                      60                      65
237 aag tgg cag ctg aag cgg gac aag cca gtg acc gtg gtg cag tcc att      298
238 Lys Trp Gln Leu Lys Arg Asp Lys Pro Val Thr Val Val Gln Ser Ile
239      70                      75                      80
241 ggc aca gag gtc atc ggc acc ctg cgg cct gac tat cga gac cgt atc      346
242 Gly Thr Glu Val Ile Gly Thr Leu Arg Pro Asp Tyr Arg Asp Arg Ile
243      85                      90                      95
245 cga ctc ttt gaa aat ggc tcc ctg ctt ctc agc gac ctg cag ctg gcc      394
246 Arg Leu Phe Glu Asn Gly Ser Leu Leu Leu Ser Asp Leu Gln Leu Ala
247 100                      105                      110                      115
249 gat gag ggc acc tat gag gtc gag atc tcc atc acc gac gac acc ttc      442
250 Asp Glu Gly Thr Tyr Glu Val Glu Ile Ser Ile Thr Asp Asp Thr Phe
251      120                      125                      130
253 act ggg gag aag acc atc aac ctt act gta gat gtg ccc att tcg agg      490
254 Thr Gly Glu Lys Thr Ile Asn Leu Thr Val Asp Val Pro Ile Ser Arg
255      135                      140                      145
257 cca cag gtg ttg gtg gct tca acc act gtg ctg gag ctc agc gag gcc      538
258 Pro Gln Val Leu Val Ala Ser Thr Thr Val Leu Glu Leu Ser Glu Ala
259      150                      155                      160
261 ttc acc ttg aac tgc tca cat gag aat ggc acc aag ccc agc tac acc      586
262 Phe Thr Leu Asn Cys Ser His Glu Asn Gly Thr Lys Pro Ser Tyr Thr
263      165                      170                      175
265 tgg ctg aag gat ggc aag ccc ctc ctc aat gac tcg aga atg ctc ctg      634
266 Trp Leu Lys Asp Gly Lys Pro Leu Leu Asn Asp Ser Arg Met Leu Leu
267 180                      185                      190                      195
269 tcc ccc gac caa aag gtg ctc acc atc acc cgc gtg ctc atg gag gat      682
270 Ser Pro Asp Gln Lys Val Leu Thr Ile Thr Arg Val Leu Met Glu Asp
271      200                      205                      210
273 gac gac ctg gac agc tgc gtg gtg gaa aac ccc atc aac cag ggc cgg      730
274 Asp Asp Leu Asp Ser Cys Val Val Glu Asn Pro Ile Asn Gln Gly Arg
275      215                      220                      225
277 acc ctg cct tgt aag atc acc gta tac aaa aaa agc tcc ttt tac ata      778
278 Thr Leu Pro Cys Lys Ile Thr Val Tyr Lys Lys Ser Ser Phe Tyr Ile
279      230                      235                      240
281 att tgt ctc aag gag gca tct tcc tcc ttt gga cct tgg tgaaga      823
282 Ile Cys Leu Lys Glu Ala Ser Ser Ser Phe Gly Pro Trp
283      245                      250                      255
286 <210> SEQ ID NO: 3
287 <211> LENGTH: 1245

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## RAW SEQUENCE LISTING

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Output Set: N:\CRF4\01312006\J520299.raw

288 &lt;212&gt; TYPE: DNA

289 &lt;213&gt; ORGANISM: Homo sapiens

291 &lt;220&gt; FEATURE:

292 &lt;221&gt; NAME/KEY: CDS

293 &lt;222&gt; LOCATION: (335)..(1147)

294 &lt;223&gt; OTHER INFORMATION:

W--&gt; 297 &lt;400&gt; 3

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298 cagatcctca tctccctggg tagtgaggct cagcacagac aagcaaccaa ctgctgggct      60
300 gccggtgccc cccatgttgg aacctgagtt ggagattatc tcctaagcag atacctgctt      120
302 ccaaactggg gatgtagggc ttggaaacta gaaaatgcca ggtctgaggg agaggaaaga      180
304 acaagtccag caatacacag agctctgtgt attcagaggg aagttggcag gggtgtgttc      240
306 gggcagagaa actccgagtg gtacaaaggg gacgtgcccc gagtggagaa atcatgctaa      300
308 ttgtctgcac tagagctgga gaacgccacc caaa atg aag aga gaa agg gga gcc      355
309                                     Met Lys Arg Glu Arg Gly Ala
310                                     1                               5
312 ctg tcc aga gcc tcc agg gcc ctg cgc ctt gct cct ttt gtc tac ctt      403
313 Leu Ser Arg Ala Ser Arg Ala Leu Arg Leu Ala Pro Phe Val Tyr Leu
314          10                      15                      20
316 ctt ctg atc cag aca gac ccc ctg gag ggg gtg aac atc acc agc ccc      451
317 Leu Leu Ile Gln Thr Asp Pro Leu Glu Gly Val Asn Ile Thr Ser Pro
318      25                      30                      35
320 gtg cgc ctg atc cat ggc acc gtg ggg aag tcg gct ctg ctt tct gtg      499
321 Val Arg Leu Ile His Gly Thr Val Gly Lys Ser Ala Leu Leu Ser Val
322 40                      45                      50                      55
324 cag tac agc agt acc agc agc gac agg cct gta gtg aag tgg cag ctg      547
325 Gln Tyr Ser Ser Thr Ser Ser Asp Arg Pro Val Val Lys Trp Gln Leu
326          60                      65                      70
328 aag cgg gac aag cca gtg acc gtg gtg cag tcc att ggc aca gag gtc      595
329 Lys Arg Asp Lys Pro Val Thr Val Val Gln Ser Ile Gly Thr Glu Val
330          75                      80                      85
332 atc ggc acc ctg cgg cct gac tat cga gac cgt atc cga ctc ttt gaa      643
333 Ile Gly Thr Leu Arg Pro Asp Tyr Arg Asp Arg Ile Arg Leu Phe Glu
334          90                      95                      100
336 aat ggc tcc ctg ctt ctc agc gac ctg cag ctg gcc gat gag ggc acc      691
337 Asn Gly Ser Leu Leu Leu Ser Asp Leu Gln Leu Ala Asp Glu Gly Thr
338      105                      110                      115
340 tat gag gtc gag atc tcc atc acc gac gac acc ttc act ggg gag aag      739
341 Tyr Glu Val Glu Ile Ser Ile Thr Asp Asp Thr Phe Thr Gly Glu Lys
342 120                      125                      130                      135
344 acc atc aac ctt act gta gat gtg ccc att tcg agg cca cag gtg ttg      787
345 Thr Ile Asn Leu Thr Val Asp Val Pro Ile Ser Arg Pro Gln Val Leu
346          140                      145                      150
348 gtg gct tca acc act gtg ctg gag ctc agc gag gcc ttc acc ttg aac      835
349 Val Ala Ser Thr Thr Val Leu Glu Leu Ser Glu Ala Phe Thr Leu Asn
350          155                      160                      165
352 tgc tca cat gag aat ggc acc aag ccc agc tac acc tgg ctg aag gat      883
353 Cys Ser His Glu Asn Gly Thr Lys Pro Ser Tyr Thr Trp Leu Lys Asp
354          170                      175                      180
356 ggc aag ccc ctc ctc aat gac tcg aga atg ctc ctg tcc ccc gac caa      931

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RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/520,299

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Input Set : E:\HYS-B2 PCT Sequence Listing.txt  
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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; Xaa Pos. 2,3  
Seq#:16; Xaa Pos. 4,5,7,8  
Seq#:17; N Pos. 676,724,742,755,769,824  
Seq#:38; N Pos. 1096,1123  
Seq#:106; Xaa Pos. 3,4

**Invalid Line Length:**

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 10

## VERIFICATION SUMMARY

DATE: 01/31/2006

PATENT APPLICATION: US/10/520,299

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L:14 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:161 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:158  
L:216 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:213  
L:297 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:294  
L:592 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:589  
L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
L:1260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0  
L:1281 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:1272  
L:1324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:618  
M:341 Repeated in SeqNo=17  
L:1448 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:1445  
L:1606 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:1603  
L:1776 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:1773  
L:1978 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:33,Line#:1975  
L:2260 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:1080  
L:2444 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:43,Line#:2441  
L:2816 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:49,Line#:2813  
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L:4829 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:96,Line#:4826  
L:5290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:106 after pos.:0